


L Number	Hits	Search Text	DB	Time stamp
1	191	urotensin	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:49
2	131449	mammal\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:49
3	114	urotensin and mammal\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:49
4	39860	hypertens\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:49
5	70	(urotensin and mammal\$) and hypertens\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:54
6	95	urotensin adj II	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 08:54
7	61	hypertens\$ and (urotensin adj II)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 09:05
8	11949	neurodegen\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 09:05
9	39	(urotensin adj II) and neurodegen\$	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/03/10 09:05

(FILE 'HOME' ENTERED AT 09:12:47 ON 10 MAR 2003)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, CANCERLIT' ENTERED AT 09:13:04 ON
10 MAR 2003

L1 879 S UROTENSIN II
L2 6 S NEURODGEN?
L3 52983 S NEURODEGEN?
L4 1 S L1 AND L3
L5 2947506 S NEURO?
L6 379 S L1 AND L5
L7 7240298 S DISEASE
L8 236783 S TRAUMA
L9 37 S L6 AND L7
L10 1 S L6 AND L8
L11 31 DUP REM L9 (6 DUPLICATES REMOVED)
L12 1061050 S ANTAGONIST?
L13 113 S L1 AND L12
L14 67 DUP REM L13 (46 DUPLICATES REMOVED)
L15 5 S L14 NOT PY>1998

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General information about the entry

Entry name	UR2_MOUSE
Primary accession number	Q9QZQ3
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	Urotensin II [Precursor]
Synonyms	U-II UII
Gene name	UTS2
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

References

[1] SEQUENCE FROM NUCLEIC ACID.
TISSUE=Spinal cord;
MEDLINE=99416011; PubMed=10486557; [NCBI, ExPASy, EBI, Israel, Japan]
Coulouarn Y., Jegou S., Tostivint H., Vaudry H., Lihmann I.;
"Cloning, sequence analysis and tissue distribution of the mouse and rat urotensin II precursors.";
FEBS Lett. 457:28-32(1999).

Comments

- **FUNCTION:** HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).
- **SUBCELLULAR LOCATION:** Secreted.
- **TISSUE SPECIFICITY:** BRAIN-SPECIFIC. PREDOMINANTLY EXPRESSED IN MOTONEURONS OF THE BRAINSTEM AND SPINAL CORD.
- **SIMILARITY:** BELONGS TO THE UROTENSIN 2 FAMILY.

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Cross-references

EMBL	AF172175; AAD55767.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
MGD	MGI:1346329; Uts2.
GeneLynx	UTS2; Mus musculus.
SOURCE	UTS2; Mus musculus.
Ensembl	Q9QZQ3; Mus musculus. [Entry / Contig view]
InterPro	IPR001483; Urotensin_II. Graphical view of domain structure.
Pfam	PF02083; Urotensin_II; 1.
PROSITE	PS00984; UROTENSIN_II; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q9QZQ3.
ProtoNet	Q9QZQ3.
ProtoMap	Q9QZQ3.
PRESAGE	Q9QZQ3.
DIP	Q9QZQ3.
ModBase	Q9QZQ3.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords**Hormone; Cleavage on pair of basic residues; Signal.****Features**

Key	From	To	Length	Description
SIGNAL	1	20	20	POTENTIAL.
PROPEP	21	104	84	POTENTIAL.
PEPTIDE	110	123	14	UROTENSIN II.
DISULFID	117	122		BY SIMILARITY.

[Feature aligner](#)[Feature table viewer](#)**Sequence information**

Length: **123 AA** [This is the length of the unprocessed precursor] Molecular weight: **13625 Da** [This is the MW of the unprocessed precursor] CRC64: **F96486195137F7F4** [This is a checksum on the sequence]

10	20	30	40	50	60
MDRV	PFCCLL	FIGLLNPLLS	LPVTD	TGERT	LQLPVLEEDA
70	80	90	100	110	120
GTEAG	ESPG	AGPSTETPTP	RGSMRKAFAG	QNSNTVLSRL	LARTRKQHKQ
					HGAAPECFWK

YCI

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or at [NCBI \(USA\)](#)Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)[ScanProsite](#), [MotifScan](#)Search the [SWISS-MODEL Repository](#)

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[\[Cross-references\]](#)
[\[Keywords\]](#)
[\[Features\]](#)
[\[Sequence\]](#)
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General information about the entry

Entry name	UR2_RAT
Primary accession number	Q9QZQ4
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 40, October 2001
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 40, October 2001

Name and origin of the protein

Protein name	Urotensin II [Precursor]
Synonyms	U-II UII
Gene name	UTS2
From	<i>Rattus norvegicus</i> (Rat) [TaxID: 10116]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

References

[1] SEQUENCE FROM NUCLEIC ACID.
 TISSUE=Spinal cord;
 MEDLINE=99416011; PubMed=10486557; [NCBI, ExPASy, EBI, Israel, Japan]
 Coulouarn Y., Jegou S., Tostivint H., Vaudry H., Lihrmann I.;
 "Cloning, sequence analysis and tissue distribution of the mouse and rat urotensin II precursors.";
 FEBS Lett. 457:28-32(1999).

Comments

- **FUNCTION:** HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).
- **SUBCELLULAR LOCATION:** Secreted.
- **TISSUE SPECIFICITY:** Brain-specific.
- **SIMILARITY:** BELONGS TO THE UROTENSIN 2 FAMILY.

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Cross-references

EMBL	AF172174; AAD55766.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR001483; Urotensin_II. Graphical view of domain structure.
Pfam	PF02083; Urotensin_II; 1.
PROSITE	PS00984; UROTENSIN_II; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q9QZQ4 .
ProtoNet	Q9QZQ4 .
ProtoMap	Q9QZQ4 .
PRESAGE	Q9QZQ4 .
DIP	Q9QZQ4 .
ModBase	Q9QZQ4 .
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords**Hormone; Cleavage on pair of basic residues; Signal.****Features**

Key	From	To	Length	Description
SIGNAL	1	20	20	POTENTIAL.
PROPEP	21	104	84	POTENTIAL.
PEPTIDE	110	123	14	UROTENSIN II.
DISULFID	117	122		BY SIMILARITY.


[Feature aligner](#)[Feature table viewer](#)**Sequence information**

Length: 123 AA [This is the length of the unprocessed precursor] Molecular weight: 13614 Da [This is the MW of the unprocessed precursor] CRC64: E4F1A8EE124AF1EA [This is a checksum on the sequence]

10	20	30	40	50	60
MDRV	PFCCLL	FVGLLNPLLS	FPVTD	TGEMS	LQLPVLEENA
70	80	90	100	110	120
GTEA	EGSLGQ	ADPSAETPTP	RGSLRKALTG	QDSNTVLSRL	LARTRKQRKQ
					HGTAPECFWK

YCI

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or at [NCBI \(USA\)](#)Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#), [Dotlet \(Java\)](#)[ScanProsite](#), [MotifScan](#)Search the [SWISS-MODEL Repository](#)[ExPASy Home page](#)[Site Map](#)[Search ExPASy](#)[Contact us](#)[Swiss-Prot](#)Hosted by [NCSC US](#) Mirror sites: [Canada](#) [China](#) [Korea](#) [Taiwan](#) [USA](#)

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General information about the entry

Entry name **UR2_HUMAN**
 Primary accession number **O95399**
 Secondary accession number **Q9UKP7**
 Entered in Swiss-Prot in **Release 40, October 2001**
 Sequence was last modified in **Release 40, October 2001**
 Annotations were last modified in **Release 41, February 2003**

Name and origin of the protein

Protein name **Urotensin II [Precursor]**
 Synonyms **U-II
UII**
 Gene name **UTS2**
 From **Homo sapiens (Human) [TaxID: 9606]**
 Taxonomy **Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.**

References

[1] SEQUENCE FROM NUCLEIC ACID.

TISSUE=Spinal cord;

MEDLINE=99080095; PubMed=9861051; [NCBI, ExPASy, EBI, Israel, Japan]

Coulouarn Y., Lihrmann I., Jegou S., Anouar Y., Tostivint H., Beauvillain J.C., Conlon J.M., Bern H.A., Vaudry H.;

"Cloning of the cDNA encoding the urotensin II precursor in frog and human reveals intense expression of the urotensin II gene in motoneurons of the spinal cord.";

Proc. Natl. Acad. Sci. U.S.A. 95:15803-15808(1998).

[2] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=99427933; PubMed=10499587; [NCBI, ExPASy, EBI, Israel, Japan]

Ames R.S., Sarau H.M., Chambers J.K., Willette R.N., Aiyar N.V., Romanic A.M., Loudon C.S., Foley J.J., Sauermelch C.F., Coatney R.W., Ao Z., Disa J., Holmes S.D., Stadel J.M., Martin J.D., Liu W.-S., Glover G.I., Wilson S., McNulty D.E., Ellis C.E., Elshourbagy N.A., Shabon U., Trill J.J., Hay D.W.P., Ohlstein E.H., Bergsma D.J., Douglas S.A.;

"Human urotensin-II is a potent vasoconstrictor and agonist for the orphan receptor GPR14.";

Nature 401:282-286(1999).

[3] SEQUENCE FROM NUCLEIC ACID.

Pearce A.;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

Comments

- **FUNCTION:** HIGHLY POTENT VASOCONSTRICTOR.
- **SUBCELLULAR LOCATION:** Secreted.
- **TISSUE SPECIFICITY:** Brain-specific.
- **SIMILARITY:** BELONGS TO THE UROTENSIN 2 FAMILY.

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Cross-references

EMBL	AF104118; AAD13070.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AF140630; AAD55577.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] Z98884; CAB63148.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
Genew	HGNC:12636 ; UTS2.
CleanEx	HGNC:12636 ; UTS2.
MIM	604097 [NCBI / EBI].
GeneCards	UTS2 .
GeneLynx	UTS2 ; Homo sapiens.
SOURCE	UTS2 ; Homo sapiens.
Ensembl	O95399; Homo sapiens. [Entry / Contig view]
InterPro	IPR001483 ; Urotensin_II. Graphical view of domain structure .
Pfam	PF02083 ; Urotensin_II; 1.
PROSITE	PS00984 ; UROTENSIN_II; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain] .
BLOCKS	O95399 .
ProtoNet	O95399 .
ProtoMap	O95399 .
PRESAGE	O95399 .
DIP	O95399 .
ModBase	O95399 .
SWISS-2DPAGE	Get region on 2D PAGE .

Keywords

Hormone; **Cleavage on pair of basic residues**; **Signal**.

Features

Key	From	To	Length	Description
SIGNAL	1	20	20	POTENTIAL.
PROPEP	21	110	90	
PEPTIDE	114	124	11	UROTENSIN II.
DISULFID	118	123		BY SIMILARITY.
CONFLICT	1	19		MYKLASCCLLFIGFLNPLL -> METNVFHLMLCVTSARTH KSTSLCFGHFNSYP (IN REF. 2).
CONFLICT	24	27		LDSR -> IHDL LL (IN REF. 2).



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Sequence information

Length: **124 AA** [This is the length of the unprocessed precursor] Molecular weight: **14295 Da** [This is the MW of the unprocessed precursor] CRC64: **C7A5FC7EFE00D312** [This is a checksum on the sequence]

10	20	30	40	50	60
MYKLASCCLL	FIGFLNPLLS	LPLLD SREIS	FQLSAPHEDA	RLTPEELERA	SLLQILPEML
70	80	90	100	110	120
GAERGDILRK	ADSSTNIFNP	RGNLRKFQDF	SGQDPNILLS	HLLARIWKPY	KKRETPDCFW

KYCV

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or at [NCBI \(USA\)](#)



Sequence analysis tools: [ProtParam](#), [ProtScale](#), [Compute pI/Mw](#), [PeptideMass](#), [PeptideCutter](#), [Dotlet](#) (Java)



[ScanProsite](#), [MotifScan](#)



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General information about the entry

Entry name **UR2R_RAT**
 Primary accession number **P49684**
 Secondary accession number **P48041**
 Entered in Swiss-Prot in **Release 33, February 1996**
 Sequence was last modified in **Release 38, July 1999**
 Annotations were last modified in **Release 41, February 2003**

Name and origin of the protein

Protein name **Urotensin II receptor**
 Synonyms **UR-II-R**
G protein-coupled sensory epithelial neuropeptide-like receptor
SENR
 Gene name **GPR14**
 From ***Rattus norvegicus* (Rat) [TaxID: 10116]**
 Taxonomy **[Eukaryota](#); [Metazoa](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Euteleostomi](#); [Mammalia](#); [Eutheria](#); [Rodentia](#); [Sciurognathi](#); [Muridae](#); [Murinae](#); [Rattus](#).**

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 MEDLINE=96115583; PubMed=8666380; [NCBI, ExPASy, EBI, Israel, Japan]
[Marchese A.](#), [Heiber M.](#), [Nguyen T.](#), [Heng H.H.Q.](#), [Saldivia V.R.](#), [Cheng R.](#), [Murphy P.M.](#), [Tsui L.-C.](#), [Shi X.](#), [Gregor P.](#), [George S.R.](#), [O'Dowd B.F.](#), [Docherty J.M.](#);
 "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10, and GPR14, encoding receptors related to interleukin 8, neuropeptide Y, and somatostatin receptors.";
[Genomics](#) 29:335-344(1995).
- [2] SEQUENCE FROM NUCLEIC ACID.
 TISSUE=[Circumvallate papillae](#);
 STRAIN=[Sprague-Dawley](#);
 MEDLINE=95251679; PubMed=7733947; [NCBI, ExPASy, EBI, Israel, Japan]
[Tal M.](#), [Ammar D.A.](#), [Karpuz M.](#), [Krizhanovsky V.](#), [Naim M.](#), [Thompson D.A.](#);
 "A novel putative neuropeptide receptor expressed in neural tissue, including sensory epithelia.";
[Biochem. Biophys. Res. Commun.](#) 209:752-759(1995).
- [3] SEQUENCE FROM NUCLEIC ACID.
 TISSUE=[Urinary bladder](#);
 STRAIN=[Wistar](#);
[Suga H.](#), [Takao K.](#);
 "Expression of the rat SENR in the urinary bladder tissues.";
 Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
- [4] SEQUENCE FROM NUCLEIC ACID.
 TISSUE=[Pheochromocytoma](#);
[Liu H.](#), [Zou M.](#), [Suga H.](#), [Takao K.](#);
 "The SENR/GPR14 expresses in rat pheochromocytoma PC 12 cells.";
 Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

Comments

- **FUNCTION:** HIGH AFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (*BY SIMILARITY*).
- **SUBCELLULAR LOCATION:** Integral membrane protein.
- **TISSUE SPECIFICITY:** PREFERENTIALLY EXPRESSED IN NEURAL AND SENSORY TISSUES.
- **SIMILARITY:** BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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Cross-references

EMBL	U32673; AAC52593.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	U23483; AAA80111.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AB012210; BAA25251.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AB029611; BAA82357.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR000276; GPCR_Rhodpsn. Graphical view of domain structure.
Pfam	PF00001; 7tm_1; 1.
PRINTS	PR00237; GPCRRHODOPSN.
PROSITE	PS00237; G_PROTEIN_RECEP_F1_1; 1. PS50262; G_PROTEIN_RECEP_F1_2; 1.
GPCRDB	P49684; UR2R_RAT.
GPCRDB-Snakes	P49684.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	P49684.
ProtoNet	P49684.
ProtoMap	P49684.
PRESAGE	P49684.
DIP	P49684.
ModBase	P49684.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

G-protein coupled receptor; Transmembrane; Glycoprotein.

Features

Key	From	To	Length	Description
DOMAIN	1	54	54	EXTRACELLULAR (<i>POTENTIAL</i>) .
TRANSMEM	55	77	23	1 (<i>POTENTIAL</i>) .
DOMAIN	78	87	10	CYTOPLASMIC (<i>POTENTIAL</i>) .
TRANSMEM	88	113	26	2 (<i>POTENTIAL</i>) .
DOMAIN	114	124	11	EXTRACELLULAR (<i>POTENTIAL</i>) .
TRANSMEM	125	146	22	3 (<i>POTENTIAL</i>) .
DOMAIN	147	167	21	CYTOPLASMIC (<i>POTENTIAL</i>) .
TRANSMEM	168	186	19	4 (<i>POTENTIAL</i>) .
DOMAIN	187	209	23	EXTRACELLULAR (<i>POTENTIAL</i>) .
TRANSMEM	210	232	23	5 (<i>POTENTIAL</i>) .
DOMAIN	233	258	26	CYTOPLASMIC (<i>POTENTIAL</i>) .
TRANSMEM	259	284	26	6 (<i>POTENTIAL</i>) .
DOMAIN	285	299	15	EXTRACELLULAR (<i>POTENTIAL</i>) .
TRANSMEM	300	321	22	7 (<i>POTENTIAL</i>) .
DOMAIN	322	386	65	CYTOPLASMIC (<i>POTENTIAL</i>) .
CARBOHYD	29	29		N-LINKED (GLCNAC...) (<i>POTENTIAL</i>) .
CARBOHYD	33	33		N-LINKED (GLCNAC...) (<i>POTENTIAL</i>) .
DISULFID	123	199		BY SIMILARITY.
CONFLICT	315	315		F -> L (IN REF. <u>1</u>) .


[Feature aligner](#)

[Feature table viewer](#)

Sequence information

Length: 386 AA Molecular weight: 42707 Da CRC64: FA4E95CC6A4CA27C [This is a checksum on the sequence]

10	20	30	40	50	60
MALSLESTTS	FHMLTVSGST	VTLPDGSNV	SLNSSWSGPT	DPSSLKDLVA	TGVIGAVLSA
70	80	90	100	110	120
MGVVGMVGNV	YTLVVMCRFL	RASASMYVYV	VNLALADLLY	LLSIPFIIAT	YVTKDWHFGD
130	140	150	160	170	180
VGCRVLFSLD	FLTMHASIFT	LTIMSSERYA	AVLRPLDTVQ	RSKGYRKLLV	LGTWLLALLL
190	200	210	220	230	240
TLPMMLAIQL	VRRGSKSLCL	PAWGPRAHRT	YLTLFPGTSI	VGPGLVIGLL	YVRLARAYWL
250	260	270	280	290	300
SQQASFKQTR	RLPNPRVLYL	ILGIVLLFWA	CFLPFWLWQL	LAQYHEAMPL	TPETARIVNY
310	320	330	340	350	360
LTTCLTYGNS	CINPFLYTLL	TKNYREYLRG	RQRSLGSSCH	SPGSPGSFLP	SRVHLQQDSG
370	380				
RSLSSSSQA	TETLMLSPVP	RNGALL			

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General information about the entry

Entry name **UR2R_HUMAN**
 Primary accession number **Q9UKP6**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 40, October 2001
 Sequence was last modified in Release 40, October 2001
 Annotations were last modified in Release 40, October 2001

Name and origin of the protein

Protein name **Urotensin II receptor**
 Synonym **UR-II-R**
 Gene name **GPR14**
 From **Homo sapiens (Human)** [TaxID: 9606]
 Taxonomy **Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.**

References

[1] SEQUENCE FROM NUCLEIC ACID.
 MEDLINE=99427933; PubMed=10499587; [NCBI, ExPASy, EBI, Israel, Japan]
[Ames R.S.](#), [Sarau H.M.](#), [Chambers J.K.](#), [Willette R.N.](#), [Aiyar N.V.](#), [Romanic A.M.](#), [Louden C.S.](#), [Foley J.J.](#), [Sauermelch C.F.](#), [Coatney R.W.](#), [Ao Z.](#), [Disa J.](#), [Holmes S.D.](#), [Stadel J.M.](#), [Martin J.D.](#), [Liu W.-S.](#), [Glover G.L.](#), [Wilson S.](#), [McNulty D.E.](#), [Ellis C.E.](#), [Elshourbagy N.A.](#), [Shabon U.](#), [Trill J.J.](#), [Hay D.W.P.](#), [Ohlstein E.H.](#), [Bergsma D.J.](#), [Douglas S.A.](#);
 "Human urotensin-II is a potent vasoconstrictor and agonist for the orphan receptor GPR14.";
 Nature 401:282-286(1999).

Comments

- **FUNCTION:** HIGH AFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
- **SUBCELLULAR LOCATION:** Integral membrane protein.
- **TISSUE SPECIFICITY:** MOST ABUNDANT EXPRESSION IN THE HEART AND PANCREAS.
- **SIMILARITY:** BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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Cross-references

EMBL	AF140631; AAD55578.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
Genew	HGNC:4468 ; GPR14.
CleanEx	HGNC:4468 ; GPR14.
MIM	600896 [NCBI / EBI].
GeneCards	GPR14 .
GeneLynx	GPR14 ; Homo sapiens.
SOURCE	GPR14 ; Homo sapiens.
Ensembl	Q9UKP6 ; Homo sapiens. [Entry / Contig view]
InterPro	IPR000276 ; GPCR_Rhodpsn. Graphical view of domain structure .
Pfam	PF00001 ; 7tm_1; 1.
PRINTS	PR00237 ; GPCRRHODOPSN.
PROSITE	PS00237 ; G_PROTEIN_RECEP_F1_1; 1. PS50262 ; G_PROTEIN_RECEP_F1_2; 1.
GPCRDB	Q9UKP6 ; UR2R_HUMAN.
GPCRDB-Snakes	Q9UKP6 .
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q9UKP6 .
ProtoNet	Q9UKP6 .
ProtoMap	Q9UKP6 .
PRESAGE	Q9UKP6 .
DIP	Q9UKP6 .
ModBase	Q9UKP6 .
SWISS-2DPAGE	Get region on 2D PAGE .

Keywords**G-protein coupled receptor; Transmembrane; Glycoprotein.****Features**

Key	From	To	Length	Description
DOMAIN	1	54	54	EXTRACELLULAR (<i>POTENTIAL</i>) .
TRANSMEM	55	77	23	1 (<i>POTENTIAL</i>) .
DOMAIN	78	87	10	CYTOPLASMIC (<i>POTENTIAL</i>) .
TRANSMEM	88	113	26	2 (<i>POTENTIAL</i>) .
DOMAIN	114	124	11	EXTRACELLULAR (<i>POTENTIAL</i>) .
TRANSMEM	125	146	22	3 (<i>POTENTIAL</i>) .
DOMAIN	147	167	21	CYTOPLASMIC (<i>POTENTIAL</i>) .
TRANSMEM	168	186	19	4 (<i>POTENTIAL</i>) .
DOMAIN	187	209	23	EXTRACELLULAR (<i>POTENTIAL</i>) .
TRANSMEM	210	232	23	5 (<i>POTENTIAL</i>) .
DOMAIN	233	258	26	CYTOPLASMIC (<i>POTENTIAL</i>) .
TRANSMEM	259	284	26	6 (<i>POTENTIAL</i>) .
DOMAIN	285	297	13	EXTRACELLULAR (<i>POTENTIAL</i>) .
TRANSMEM	298	318	21	7 (<i>POTENTIAL</i>) .
DOMAIN	319	389	71	CYTOPLASMIC (<i>POTENTIAL</i>) .
CARBOHYD	29	29		N-LINKED (GLCNAC...) (<i>POTENTIAL</i>) .
CARBOHYD	33	33		N-LINKED (GLCNAC...) (<i>POTENTIAL</i>) .
DISULFID	123	199		BY SIMILARITY.

[Feature aligner](#)[Feature table viewer](#)**Sequence information**

Length: 389 AA Molecular weight: 42130 Da CRC64: 6D6A88DBF78400CE [This is a checksum on the sequence]


```

      10           20           30           40           50           60
MALTPESPSS FPGLAATGSS VPEPPGGPNA TLNSSWASPT EPSSLEDLVA TGTIGTLLSA

      70           80           90          100          110          120
MGVVGVVGN YTLVVTCRSL RAVASMYVYV VNLALADLLY LLSIPFIVAT YVTKEWHFGD

     130          140          150          160          170          180
VGCRVLFGLD FLTMHASIFT LTMSSERYA AVLRPLDTVQ RPKGYRKLLA LGTWLLALLL

     190          200          210          220          230          240
TLPVMLAMRL VRRGPKSLCL PAWGPAHRA YLTLLFATSI AGPGLLIGLL YARLARAYRR

     250          260          270          280          290          300
SQRASFKRAR RPGARALRLV LGIVLLFWAC FLPFWLWQLL AQYHQAPLAP RTARIVNYLT

     310          320          330          340          350          360
TCLTYGNSCA NPFLYTLLTR NYRDHLRGRV RGPSSGGGRG PVPSLQPRAR FQRCSGRSLS

     370          380
SCSPQPTDSL VLAPAAPARP APEGPRAPA

```

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General information about the entry

Entry name	UR2R_BOVIN
Primary accession number	P49220
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 33, February 1996
Sequence was last modified in	Release 33, February 1996
Annotations were last modified in	Release 40, October 2001

Name and origin of the protein

Protein name	Urotensin II receptor [Fragment]
Synonyms	UR-II-R G protein-coupled sensory epithelial neuropeptide-like receptor SENR
Gene name	GPR14
From	<i>Bos taurus</i> (Bovine) [TaxID: 9913]
Taxonomy	Eukaryota ; Metazoa ; Chordata ; Craniata ; Vertebrata ; Euteleostomi ; Mammalia ; Eutheria ; Cetartiodactyla ; Ruminantia ; Pecora ; Bovoidea ; Bovidae ; Bovinae ; Bos .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 TISSUE=Retina;
 MEDLINE=95251679; PubMed=7733947; [NCBI, ExPASy, EBI, Israel, Japan]
 Tal M., Ammar D.A., Karpui M., Krizhanovsky V., Naim M., Thompson D.A.;
 "A novel putative neuropeptide receptor expressed in neural tissue, including sensory epithelia."
 Biochem. Biophys. Res. Commun. 209:752-759(1995).

Comments

- **FUNCTION:** HIGH AFINITY RECEPTOR FOR UROTENSIN II. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (*BY SIMILARITY*).
- **SUBCELLULAR LOCATION:** Integral membrane protein.
- **TISSUE SPECIFICITY:** EXPRESSED IN NEURAL TISSUE, INCLUDING SENSORY EPITHELIA.
- **SIMILARITY:** BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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Cross-references

EMBL	U23459; AAC48464.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR000276; GPCR_Rhodpsn. Graphical view of domain structure.
Pfam	PF00001; 7tm_1; 1.
PRINTS	PR00237; GPCRRHODOPSN.
PROSITE	PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL. PS50262; G_PROTEIN_RECEP_F1_2; 1.
BLOCKS	P49220.
ProtoNet	P49220.
ProtoMap	P49220.
PRESAGE	P49220.
DIP	P49220.
ModBase	P49220.
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Keywords**G-protein coupled receptor; Transmembrane; Glycoprotein.****Features**

Key	From	To	Length	Description
NON_TER	1	1		
TRANSMEM	<1	16	>16	2 (POTENTIAL).
DOMAIN	17	27	11	EXTRACELLULAR (POTENTIAL).
TRANSMEM	28	49	22	3 (POTENTIAL).
DOMAIN	50	70	21	CYTOPLASMIC (POTENTIAL).
TRANSMEM	71	89	19	4 (POTENTIAL).
DOMAIN	90	111	22	EXTRACELLULAR (POTENTIAL).
TRANSMEM	112	135	24	5 (POTENTIAL).
DOMAIN	136	161	26	CYTOPLASMIC (POTENTIAL).
TRANSMEM	162	187	26	6 (POTENTIAL).
DOMAIN	188	194	7	EXTRACELLULAR (POTENTIAL).
TRANSMEM	195	215	21	7 (POTENTIAL).
DISULFID	26	102		POTENTIAL.
NON_TER	215	215		

[Feature aligner](#)[Feature table viewer](#)**Sequence information**

Length: 215 AA [This is the length of the partial sequence] Molecular weight: 24575 Da [This is the MW of the partial sequence] CRC64: 97F2D5041D96A624 [This is a checksum on the sequence]

10	20	30	40	50	60
LLYLLSIPFI	VATYVTKRWH	FGDVGCRVLF	SLDFLTMHAS	IFTLTMSRE	RYAAVVRPLD
70	80	90	100	110	120
TVQRSKGYRK	VLALGTWLLA	LLLALPMMLA	IRLVRRGHKS	LCLPAWGQRT	HRAYLTLLFG
130	140	150	160	170	180
TSIVGPGVVI	GLLYVRLARA	YWLSQRASFT	QTRRLPNPRV	LYLILGIVLL	FWACFLPFWL
190	200	210			
WQLLAQYRGA	PPLAPRSARI	VNYLTTCLTY	GNSCV		

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